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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/034,286 03/04/98 FALB

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HM12/1024

EXAMINER

NGUYEN, D

ART UNIT

PAPER NUMBER

1633

DATE MAILED:

10/24/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary

Application No.

09/034,286

Applicant(s)

Falb

Examiner

Dave Nguyen

Group Art Unit

1633



☒ Responsive to communication(s) filed on Sep 5, 2000

☐ This action is FINAL.

☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

A shortened statutory period for response to this action is set to expire 3 month(s), or thirty days, whichever is longer, from the mailing date of this communication. Failure to respond within the period for response will cause the application to become abandoned. (35 U.S.C. § 133). Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

Disposition of Claims

☒ Claim(s) 53-83 is/are pending in the application.

Of the above, claim(s) _____ is/are withdrawn from consideration.

☐ Claim(s) _____ is/are allowed.

☒ Claim(s) 53-83 is/are rejected.

☐ Claim(s) _____ is/are objected to.

☐ Claims _____ are subject to restriction or election requirement.

Application Papers

☐ See the attached Notice of Draftsperson's Patent Drawing Review, PTO-948.

☐ The drawing(s) filed on _____ is/are objected to by the Examiner.

☐ The proposed drawing correction, filed on _____ is ☐ approved ☐ disapproved.

☐ The specification is objected to by the Examiner.

☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).

☐ All ☐ Some* ☐ None of the CERTIFIED copies of the priority documents have been
☐ received.

☐ received in Application No. (Series Code/Serial Number) _____.

☐ received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

*Certified copies not received: _____

☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

Attachment(s)

☐ Notice of References Cited, PTO-892

☐ Information Disclosure Statement(s), PTO-1449, Paper No(s). _____

☐ Interview Summary, PTO-413

☐ Notice of Draftsperson's Patent Drawing Review, PTO-948

☐ Notice of Informal Patent Application, PTO-152

— SEE OFFICE ACTION ON THE FOLLOWING PAGES —

The request filed on September 5, 2000, for a Continued Prosecution Application (CPA) under 37 CFR 1.53(d) based on parent Application No. 09/034,286 is acceptable and a CPA has been established. An action on the CPA follows.

The specification has been amended by the preliminary amendment dated August 6, 1998.

Claims 53-83 are pending to which the following grounds of rejection remain and/or are applicable.

Objection to the Specification

The specification remains objected to under 37CFR 1.52(b), which requires that the pages of the specification be numbered starting with "1". Pages i-iv of the specification do not conform with the arrangement of the specification according to MPEP 608.01(a), particularly since the item (b) "Cross Reference to Related Applications" does not appear on the first paragraph of the specification, and since the title headings appear both at page i and page 1 of the specification. It is suggested that pages i-iv should be deleted or removed from the specification.

The following guidelines illustrate the preferred layout and content for patent applications. These guidelines are suggested for the applicant's use.

Arrangement of the Specification

The following order or arrangement is preferred in framing the specification and, except for the reference to a "Microfiche Appendix" and the drawings, each of the lettered items should appear in upper case, without underlining or bold type, as section headings. If no text follows the section heading, the phrase "Not Applicable" should follow the section heading:

- (a) Title of the Invention.
- (b) Cross - Reference to Related Applications.
- (c) Statement Regarding Federally Sponsored Research or Development.
- (d) Reference to a "Microfiche Appendix" (see 37 CFR 1.96).
- (e) Background of the Invention.
 - 1. Field of the Invention.
 - 2. Description of Related Art including information disclosed under 37 CFR 1.97 and 1.98.
- (f) Brief Summary of the Invention.
- (g) Brief Description of the Several Views of the Drawing(s).
- (h) Detailed Description of the Invention.

- (i) Claim or Claims (commencing on a separate sheet).
- (j) Abstract of the Disclosure (commencing on a separate sheet).
- (k) Drawings.
- (l) Sequence Listing (see 37 CFR 1.821 - 1.825).

The following is a quotation of the first paragraph of 35 U.S.C. § 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 61, 63, 65, 67-77 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 61, 63, 65, 67-77 are readable on polynucleotide sequences that hybridize under highly stringent conditions (defined) to the polynucleotide sequence of claim 54 or 56 (SEQ ID NO: 64 or SEQ ID No: 65) without any recitation of their biological functions. However, the specification only discloses a human rchd534-long gene (cDNA and/or mRNA sequences) which is down-regulated in endothelial cells under shear stress (SEQ ID NO: 64 or SEQ ID No: 65 which encoded by SEQ ID NO: 64). In analyzing whether the written description requirement is met for genus claim, it is first determined whether a representative number of species have been described by their complete structure. In this case, SEQ ID NO. 64 is the only species whose complete structure and function is disclosed. Next, then, it is determined whether a representative number of species have been sufficiently described by other relevant identifying characteristics (i.e., other than nucleotide sequence). In this case, the only identifying characteristics are the "hybridization" characteristics of the claimed genus of polynucleotide sequences. While the application and the claims recite the "hybridization" characteristics of all of the mammalian genes other than the rchd534-long gene and fragments thereof, it is not apparent how one skilled in the art determines what are exactly the sequence structures of all claimed DNA

sequences encoding functionally active polypeptides other than the rchd534-long gene, particularly since the problem of predicting protein structure from mere sequence data of a single amino acid or nucleic acid sequence of the rchd534-long gene (SEQ ID No: 64) and in turn utilizing the sequence structures to ascertain the sequence structures of all other mammalian genes that have biological function other than that of the rchd534-long gene is complex (Ngo *et al.*, in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz *et al.*, (ed.), Birkhauser, Boston, MA, pp. 492-495). This limited information is not sufficient to reasonably convey to one skilled in the art that Applicant was in possession of functionally active genes other than the rchd534-long gene (SEQ ID NO: 64) and the polynucleotide sequences as claimed in claims 62, 64, and 66.

Claims 61, 63, 65, 67-77 are rejected under 35 U.S.C. 112, first paragraph, because the specification is enabling only for claims limited to DNA sequences encoding SEQ ID NO: 65 which includes SEQ ID NO: 64, and to the DNA sequences as recited in claims 62, 64, and 66. The specification does not reasonably provide enablement for claims directed to other polynucleotide sequences as recited in the claims. The specification does not enable any person skilled in the art to which it pertains or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

When given their broadest reasonable interpretation, the claims are clearly intended to encompass a variety of species including unspecified genes encoding for an unspecified protein. However, the specification fails to provide an enabling disclosure for what such polynucleotides would comprise and how one skilled in the art determines which of the unspecified polynucleotide sequences as claimed, without undue experimentation, particularly on the basis of applicant's disclosure. While the application contemplates that all of the claimed polynucleotide sequences have a biological function or activity, the application does not provide sufficient guidance and/or evidence for one skilled in the art to determine which of the claimed polynucleotide sequences exhibits a biological function disclosed in the application. Thus, given the lack of guidance and direction in regard to what the polynucleotides defined by the claims would comprise and how one would use such, the artisan would be required to exercise undue experimentation in practice

of the invention. Note that the Court of Appeals for the Federal Circuit has ruled that claims that embrace a large number of species of polynucleotide sequences without proper guidance in the application as to how to make and use such polynucleotides do not meet the requirements of 35 U.S.C. § 112, first paragraph, *Amgen v Chugai* (18 USPQ2d 1016 (Fed. Cir. 1991)).

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 54, 57, 61, 62, and 67-77 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 54, 57 and claims dependent therefrom remain indefinite in the recitation of "the amino acid unique to the rchd534-long protein" because it is not apparent as to what are the metes and bounds of the "unique". Note that "the amino acid unique" also lacks an antecedent basis.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

- (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
- (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 54, 57, 61-66, 68-73, 75, and 77-83 remain rejected under 35 U.S.C. 102(a) as being anticipated by Imamura *et al.* (Nature 389, pp. 622-626, 1997).

The claims are directed to DNA sequences encoding the amino acid sequence set forth from amino acid number 1 to 273 in SEQ ID NO: 65 or any polynucleotide sequence that hybridizes under defined stringent conditions to the rchd534-long gene (SEQ ID NO: 64), vectors, cDNA sequences, and host cells containing the polynucleotide sequences. A method of

producing a gene product encoded by the polynucleotide sequence is also claimed in claim 77. Claims 54 and 57 also recite DNA sequence comprising a polypeptide coding region unique to the coding region of SEQ ID NO: 64. Imamura *et al.* disclose a cultured mammalian cell containing a cDNA clone having an expression vector which comprises a polynucleotide sequence (isolated from a heart cDNA library) which has 93% match to the rchd534-long gene (SEQ ID NO: 64).

Absent evidence to the contrary, the polynucleotide sequences, host cells, and vectors of Imamura *et al.* has all of the properties cited in the claims, e.g., hybridizes under the recited stringent condition, and comprise sequences being unique to the coding region of SEQ ID NO: 64.

Claims 63, 64, and 67 remain rejected under 35 U.S.C. 102(b) as being anticipated by Riggins *et al.* (Gene Bank Database, AN: U59914, published November 1, 1996).

The claims are directed to any polynucleotide sequence that that hybridizes under the recited highly stringent conditions to any polynucleotide sequence that encodes the amino acid sequence set forth in SEQ ID NO: 65.

Riggins *et al.* teach a polynucleotide sequence that encodes a Mad homolog smad6 mRNA, wherein the polynucleotide sequence (isolated and sequenced from a human chromosome) has 99.3% identity to nucleotides 972-1812 of SEQ ID NO: 64 of the application (SEQ ID NO: 64 encodes the rchd534-long protein).

Absent evidence to the contrary, the polynucleotide sequence of Riggins *et al.* hybridizes to SEQ ID NO: 64, and has all of the properties cited in the claims.

Claims 54, 57, 61-73, 75, and 77-83 remain rejected under 35 U.S.C. 102(a) as being anticipated by Hata *et al.* (Genes & Development 12, pp. 186-197, published January 15, 1998).

The claims are directed to any polynucleotide sequence that hybridizes under the recited stringent conditions. The claims are also directed to vectors, eukaryotic host cells containing the polynucleotide sequence. Claims 54 and 57 also recite DNA sequence comprising any

polypeptide coding region unique to the coding region of SEQ ID NO: 64.

Hata *et al.* teach a method using vectors and eukaryotic host cells for generating a cDNA sequence (the Smad6 gene) that encodes a polypeptide sequence which is 99.9% identical to SEQ ID NO: 65 (which is also encoded by the cDNA sequence contained in the plasmid clone pHL6T11A, pages 195 and 196) also see the search Result attached to the PTO-892 form). Methods for making recombinant proteins encoded by the Smad6 gene is also disclosed in Hata *et al.* Figure 7 at page 194 of Hata *et al.* provides evidence demonstrating that the Smad6 gene product inhibits a TGF- β signaling.

Absent evidence the contrary, the DNA sequence, vectors, host cells, methods for producing the Smad6 gene product of Hata *et al.* have all of the properties cited in the claims.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 53-83 remain rejected under 35 U.S.C. 103(a) as being unpatentable over Hata *et al.* (Genes & Development 12, pp. 186-197, published January 15, 1998) in view of Moren (Gene Bank Database, AN: AF043640, published February 4, 1998), and Blakely *et al.* (US Pat No. 5,418,162).

The claims are directed to any polynucleotide sequence that encodes the polypeptide sequence set forth in SEQ ID NO: 65, and any polynucleotide sequence that hybridizes under highly stringent conditions to the polynucleotide sequence of SEQ ID NO: 65. The claims are also directed to vectors, prokaryotic and eukaryotic host cells containing any polynucleotide sequence that encodes the polypeptide sequence set forth in SEQ ID NO: 65.

Hata *et al.* teach a method using vectors and eukaryotic host cells for generating a cDNA sequence (the Smad6 gene) that encodes a polypeptide sequence which is 99.9% identical to

SEQ ID NO: 65 (which is also encoded by the cDNA sequence contained in the plasmid clone pHL6T11A, pages 195 and 196) also see the search Result attached to the PTO-892 form). The Smad6 gene has one nucleotide mismatch, e.g., Asn → Asp, at base 997 as compared to SEQ ID NO: 64 of this application. Methods for making recombinant proteins encoded by the Smad6 gene is also disclosed in Hata *et al.* Figure 7 at page 194 of Hata *et al.* provides evidence demonstrating that the Smad6 gene product inhibits a TGF- β signaling. Hata *et al.* do not teach the exact sequences as set forth in SEQ ID Nos 64 and 65, nor do Hata *et al.* teach prokaryotic host cells containing the Smad6 gene.

However, at the time the invention was made, Moren teaches a complete mRNA sequence encoding the human Smad6 gene (obtained from chromosome 15) which has 100% match to the cDNA coding sequence set forth in SEQ ID NO: 64 or the rchd534-long gene.

In addition, Blakely *et al.* disclose that it is routine to employ prokaryotic host cells to produce recombinant proteins from a known gene (column 5, lines 35-45)

It would have been obvious to one of ordinary skill in the art at the time the invention was made that the difference by one conservative substitution in the Smad6 gene of Hata *et al.* as compared to SEQ ID NO: 64 of this application would either be the result of sequencing artifact or allelic variation, and thus, the difference is *de minimis*, particularly since the encoded polypeptide sequence of Hata *et al.* is 99.9% identical to the encoded polypeptide sequence of the rchd534-long gene (see the sequence comparison disclosed in the search results).

It would also have been obvious for one of ordinary skill in the art to have employed the Smad6 gene disclosed in Moren in the method of Hata *et al.* to produce recombinant Smad6 gene products, as taught by Hata *et al.*, with a reasonable expectation of success, particularly since both coding sequences disclosed in Moren *et al.* and Hata *et al.* encode a Smad6 gene product.

It would also have been obvious for one of ordinary skill in the art to have employed prokaryotic cells to produce Smad6 gene products in the method of Hata *et al.*, with a reasonable expectation of success, particularly since it is well known in the prior art that prokaryotic cells and eukaryotic cells are routinely employed in the art to produce recombinant proteins.

Thus, the claimed invention as a whole was *prima facie* obvious.

Claims 77-83 remain rejected under 35 U.S.C. 103(a) as being unpatentable over either Imamura *et al.* (Nature 389, pp. 622-626, 1997) or by Hata *et al.* (Genes & Development 12, pp. 186-197, published January 15, 1998) taken with either Bresser *et al.* (US Pat No. 5,225,326) or Venter *et al.* (WO 93/00353).

Hata *et al.* teach a method using vectors and eukaryotic host cells for generating a cDNA sequence (the Smad6 gene) that encodes a polypeptide sequence which is 99.9% identical to SEQ ID NO: 65 (which is also encoded by the cDNA sequence contained in the plasmid clone pHL6T11A, pages 195 and 196) also see the search Result attached to the PTO-892 form). Methods for making recombinant proteins encoded by the Smad6 gene is also disclosed in Hata *et al.* Figure 7 at page 194 of Hata *et al.* provides evidence demonstrating that the Smad6 gene product inhibits a TGF- β signaling.

Imamura *et al.* disclose a cultured mammalian cell containing a cDNA clone having an expression vector which comprises a polynucleotide sequence (isolated from a heart cDNA library) which has 93% match to the rchd534-long gene. Either Hata *et al.* or Imamura *et al.* does not teach that their disclosed DNA sequences can be employed to make DNA probes or primes consisting of at least 14 contiguous nucleotides of the nucleotide sequence from the residue number 155 to 973 of SEQ ID NO: 64.

However, at the time the invention was made, Venter *et al.* discuss the use of ESTs in sequencing and mapping the human genome (entire document). Venter *et al.* disclose that at least 15 nucleotide probes and/or primers obtained from any EST sequence are sufficient to be used as hybridization probes (p. 10, second paragraph, page 17, second paragraph, and page 26, third paragraph). Prokaryotic cells and/or eukaryotic cells containing DNA comprising a promoter operably linked to the hybridization probes, and methods using cells for producing the nucleic acid molecules are also disclosed at page 20.

In addition, Bresser *et al.* teach an *in situ* hybridization assay method for the detection of known RNA or DNA sequences in cells (the entire document). The method employs

oligonucleotides (oligos) 12-50 or 50-150 bases long (for DNA or RNA detection, respectively; columns 3 and 9, for example). The oligos may consist of DNA or RNA.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce shorter segments of the DNA sequences disclosed either Hata *et al.* or Imamura *et al.* in order to detect the genetic markers or quantities of DNA sequences in the tissue as the single cell level using the disclosure of either Venter *et al.* or Bresser *et al.* Either Venter *et al.* or Bresser *et al.* teach a method for making such nucleic acid molecules and/or host cells, and provide motivation for doing so. One of ordinary skill in the art would have been motivated to have employed in the nucleic acid molecules of either Hata *et al.* or Imamura *et al.* for making probes or primer using the method either Venter *et al.* or Bresser *et al.* in order to detect particular cells and/or tissues that contains genetic markers and/or quantities of the nucleic acid sequences disclosed in either Hata *et al.* or Imamura *et al.*

Double patenting rejection

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 63 and 67 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-7 of U.S. Patent No. 5,834,248. Although the conflicting claims are not identical, they are not patentably distinct from each other because claims 1-7 of the '248 patent recite human DNA sequences encoding SEQ ID NO: 37 (SEQ ID

NO: 36, for example) that is identical to residues 972 to 1752 of SEQ ID NO: 34 of this instant application.

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to *Dave Nguyen* whose telephone number is **(703) 305-2024**.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, *John LeGuyader*, may be reached at **(703) 308-0447**.

Any inquiry of a general nature or relating to the status of this application should be directed to the *Group receptionist* whose telephone number is **(703) 308-0196**.



Dave Nguyen

Patent Examiner

Art Unit: 1633